

OM of: US-09-494-297-2 to: GenEmbl: \* out\_format : pfs

Date: Jun 6, 2001 10:59 PM

About: Results were produced by the Gencore software, version 4.5,

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#### Command line parameters:

```
-MODEL="frame+P2n.model -DEV=xlp
-Q=/cgnl_1/USPO_spool/US09494297/runat_06062001_115734_12308/app_query.fasta_1.825
-DB=3genEmbl -QFORMAT=fastap -SUFFIX="app" -GAPOPEN=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOPEN=4.500
-QGAPEXT=0.050 -XGAPOPEN=10.000 -XGAPEXT=0.500 -FGAPOPEN=6.000
-FGAPEXT=7.000 -YGAPEXT=6.000 -DELOPEN=6.000
-DELEXT=7.000 -START=1 -MATRIX=blossom2 -TRANS=human4_cds1
-LIST=45 -DOCALIGN=200 -THR_SCOREPECT = -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFORMAT=PFS -NORMTEXT -MINLEN=0
-MAXLEN=20000000 -USERID=US09494297@CGNL_1.7604 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPEA -WAIT -THREADS=1
```

#### Search information block:

Query: US-09-494-297-2

Query length: 757

Database: GenEmbl: \*

Database sequences: 1283235

Database length: -121600440

Search time (sec): 2987.740000

#### score\_list:

Sequence	Strd	Orig	Zscore	Escore	Len	Documentation
gb_ba3:SPU49397	-	1955.50	1843.52	1.8e-94	10826	! u49397 Streptococcus pyogenes
gb_ba3:STRPINF	+	633.50	597.92	4.3e-25	2845	! L10919 Streptococcus pyogenes
gb_ba1:AF005908	+	611.00	576.82	6.5e-24	2801	! AF005908 Streptococcus pyogenes
gb_ba2:GGU3115	+	523.00	571.10	1.4e-23	2263	! XE7947 S. pyogenes f. suis 11 group G streptococcus f. suis 11 gene for fumC
gb_ba1:AF005914	+	222.50	275.93	3.7e-07	321	! AF005914 Streptococcus pyogenes
gb_ba1:AF005913	+	262.50	266.71	1.2e-06	313	! AF005913 Streptococcus pyogenes
gb_ba1:AF005910	+	241.50	246.54	1.6e-05	326	! AF005910 Streptococcus pyogenes
gb_ba1:AF005920	+	222.50	228.05	0.0002	348	! AF005920 Streptococcus pyogenes
gb_ba1:AF005917	+	211.50	219.59	0.0005	278	! AF005917 Streptococcus pyogenes
gb_ba1:AF005911	+	211.50	218.66	0.0005	310	! AF005911 Streptococcus pyogenes
gb_ba1:AF005918	+	210.50	217.74	0.0006	309	! AF005918 Streptococcus pyogenes
gb_ba1:AF005915	+	209.50	216.80	0.0007	309	! AF005915 Streptococcus pyogenes
gb_ba1:AF005912	+	205.50	213.81	0.0011	282	! AF005912 Streptococcus pyogenes
gb_ba1:AF005919	+	204.50	212.11	0.0013	308	! AF005919 Streptococcus pyogenes
gb_ba1:AF005919	+	202.50	211.01	0.0013	281	! AF005919 Streptococcus pyogenes
gb_ba1:AF005916	+	185.00	195.32	0.0115	255	! AF005916 Streptococcus pyogenes
gb_ba1:SEFNAGEN	+	180.00	172.44	0.2170	2127	! X99995 S. equi fnz gene. 1/1997
gb_ba1:AR083961	+	178.00	168.52	0.3584	2694	! AR083961 Sequence 2 from pattern
gb_ba1:AR083960	+	178.00	159.58	1.13	7650	! AR083960 Sequence 1 from pattern
gb_ba1:AF043131	+	178.00	158.24	1.34	8946	! AF043131 Moraxella catarrhalis
gb_ba1:AF067453	+	177.00	142.62	9.93	4961	! AX067453 Sequence 28 from Pat
gb_ba1:AF043133	+	176.00	166.56	0.4611	2718	! AF043133 Moraxella catarrhalis
gb_ba1:SPU31980	+	162.50	152.94	2.64	3552	! U31980 Streptococcus pyogenes
gb_ba2:AP00592	-	162.00	113.00	43.49	318850	! AP00592 Thermoplasma volvoc
gb_ba1:AF1-20104	+	160.00	140.29	13.41	1020	! AF120104 Lactobacillus reuteri
gb_ba1:LL004468	+	159.00	146.93	5.72	4133	! U04468 Lactococcus lactis sex
gb_ba1:AH139040	+	159.00	114.67	358.06	17846	! U04468 Lactococcus lactis sex
gb_ba2:BACISPN	+	155.00	141.25	11.84	5160	! D4498 Bacillus subtilis hisPN
gb_ba1:AF134726	-	155.00	110.81	587.58	180283	! AF134726 Homo sapiens BAC cl
gb_ba1:AF188483	+	152.00	135.16	25.88	7551	! AF188483 Photobacterium luminescens
gb_ba1:AP00503	-	151.50	112.56	469.73	100000	! AP00503 Homo sapiens genome
gb_ba2:CDTOKBA	+	151.00	134.67	27.57	7164	! Z23277 C.diffficile gene for tc
gb_ba1:AC05505	+	151.00	106.46	1.0e-03	192929	! AC05505 Plasmidium falciPar
gb_ba1:AC005139	-	151.00	104.03	1.4e-03	256172	! AC005139 Plasmodium falciPar
gb_ba1:AF071281	+	150.00	139.78	14.30	3531	! AF071281 Sequence 1 from pattern
gb_ba1:AF071083	+	150.00	139.39	15.05	3698	! AF071083 Streptococcus pyogenes
gb_ba1:HUMHHHSP	+	149.00	141.14	12.02	2700	! M59828 Human HHC class III HSP
gb_ba1:SAU5646	+	149.00	137.88	18.25	3948	! AJ005646 Staphylococcus aureus
gb_ba1:AR067712	+	149.00	136.55	21.65	4612	! AR067712 Sequence 8 from pattern
gb_ba3:STACNA	+	148.00	19.90	3827	1 M81736 Staphylococcus aureus	

gb_pat1:AR067706	+	148.00	137.21	19.90	3827	! AR067706 Sequence 1 from pattern
gb_ba1:AE002147	-	147.00	119.50	192.89	27093	! AE002147 Ureaplasma urealyticum
gb_pat1:A18434	+	146.00	136.16	22.75	3468	! A18434 Hybrid DNA molecule
gb_ba1:A18436	+	146.00	133.72	31.12	4612	! A18436 assembled sequence of



20 SerLysasnSerLysarg.....PheThrValIleuValGly'ValPh 34  
   |||  |||||  |||||  |||||  |||||  |||||  |||||  
 593 AGCGCTTACACAAGGGACGACAAGGGATTCGGAATCAGAACTATT 5854  
   34 eleumetilepheAlaIleuValThrSerMetValGlyAlaIleuThrValP 51  
   |||||  |||||  |||||  |||||  |||||  |||||  
 583 TTGACCGTTGTAGCTCTGATAGGAATAGGATTTCTATCAGAGCGT 5804  
   51 heglyLeuIvaIgluSerSerIhrProasnAlaIleuasnProaspSer 67  
   |||||  |||||  |||||  |||||  |||||  |||||  
 583 TCGGAGCTGAAGAACATCACTTACCAAAT.....AGACAAGCTCATT 5760  
   84 rmyrLysGlnPheArgValAlaHisaspIleuArgValAsnLeuIgluLys 101  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5709 CTATAGTCGCTTAAGGCTTACCATTAATAAGTAATTTAGGGCTA 5710  
   101 erArgSerTyrcIvnValTyrcIysPheasnLeuLysIvalAlaPhePheLeu 117  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5609 AAGTCAGATAGTGTAGATCACATGGTATAAAACTTGAGGAACTAA 5560  
   134 rThrLysPheGluAspPyrrAlaMetterProarginThrGlyAspGluL 151  
   |||||  |||||  |||||  |||||  |||||  |||||  
 559 TCAAACCTTATCAAGTAGGAGTCTCTATAATGGATACCTCTATACTG 5460  
   168 AsnGlyIleMetGluglyLeuGluProLeuAsnAlaIleArgValThrG 184  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5459 AATGGGTAATGAAAGGGATAGTCCTAAACGCCTTTAGTGACTCA 5410  
   184 ngluIalavaltryrPyrrSerAspasnAlaProIleSerasnProaspG 201  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5409 AAATGCHATTGG...TATACGATGCAATT..ATCCGGATG 5366  
   201 luserPheLysargGluSerGluSerasnLeuValSerThrSerGlnLeu 217  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5365 AAAGTTTAAACAGAACGCTCGAAGTATGGTTATATGACCGAGTTA 5316  
   218 SerLeuMetArgGlnAlaIleuIysGlnIleuIleuAspProasnLeuAla 234  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5315 GCCTTATGCGAAAGGTTAAAGAACATAATGACCAACTTAGGTC 5266  
   234 rlysmetProLysGlnValProAspaspPheinLeuSerIlePheGluS 251  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5265 AAATATTCGAATAAACCTCATCAGGTTATGGTAAATGTTGAT 5216  
   268 GlyGlyLeuValProThrLysProProThrProGlyAspProPromPr 284  
   |||||  |||||  |||||  |||||  |||||  |||||  
 521 ergluAspLysGlyAspLysTyrAspIysGlyTyrgInAspLeuIser 267  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5215 CTCATGAT.....AAGCCATTCTCAAATCTTTGAGT 5184  
   284 oProAspGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleG 301  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5139 TCGGCCAAACTGAANAAAACCTCAGCATTATCAGAAAATGCGGAG 5090  
   301 lVASPTyrsSerLysLeuIleuIgluIgluIalathLeuIleuIthrGlyAsp 317  
   |||||  |||||  |||||  |||||  |||||  |||||  
 5089 GTGAC...TCTAACTCTAGAGGGACCAACCTTAAGCTTCTCAATT 5043  
   318 AsnValAsnSerPheGlnAlaArgValPheSerSerasnAspIleGly 334

5042 GAGGAAGTGGTTTCAGAAAAGACTTCAGAATGATAGTTAGGAGA 4993  
   |||||  |||||  |||||  |||||  |||||  |||||  
 334 uArgIleGluIeuserAspGlyThrThrIleutngluteuasnSerP 351  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4992 RACTGCGAATTCCAATGGGACTTATACCTTACAGAAACATCATCTC 4943  
   |||||  |||||  |||||  |||||  |||||  |||||  
 351 roAlaGlyTyrsErleAlaGluProIleThrPheIysValGluAlaGly 367  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4942 CAGATGGATATAATGCGGGCCGATTAAGTTAGAGTAGAGAATAAA 4893  
   |||||  |||||  |||||  |||||  |||||  |||||  
 368 LysValTyrThrIle...IleasGlyLysGlnIleGluAsnProasnly 383  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4892 AAGTGTATTATCTGTCACAAAGATGGTCTCAGTGAGAAATCCAAACAA 4843  
   |||||  |||||  |||||  |||||  |||||  |||||  
 383 sGluIleValGluIproTyrsErValGluIalatyRasnaspHeGluGluP 400  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4842 AGAGTACGAGGCCATACTCGTGGAGCTTATAGCTTATGGT 4793  
   |||||  |||||  |||||  |||||  |||||  |||||  
 400 heservalLeuThr...ThrGlnAspIlyRasnaspHeTyTyralalys 415  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4792 AATAAGGATAAAAGTTCAGAAGTGTCTACTCCATACGGAAATTCATCTAC 4743  
   |||||  |||||  |||||  |||||  |||||  |||||  
 416 AsnlysasnGlySerGlnValValTyrcIysPheasnProasnAlaSpIe 432  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4742 AATAAGGATAAAAGTTCAGAAGTGTCTACTCCATACGGAAATTCATCTAC 4693  
   |||||  |||||  |||||  |||||  |||||  |||||  
 432 sSerProProaspSerGluasPpglyGlyLysIthrMetThrProaspPhe 449  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4692 CTCACACCCTGACTCATGATGATGTTGTCGACTTAAATCCAGACTA 4643  
   |||||  |||||  |||||  |||||  |||||  |||||  
 449 hThr...GlyIgluvalylsTyrrHsIleAlaIgylargAspLeuPhe 464  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4642 GTCAGATGAAAGAAGTCACACATACGGCAGGTAGTGACTGTGTT 4593  
   |||||  |||||  |||||  |||||  |||||  |||||  
 465 LysTyrrHValLysProGlyAspThrasPProaspThrPheLeuYshi 481  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4592 AATATTCGCTTAAGACCGAGATAACAATCGAAAGACTCTTAAGCA 4543  
   |||||  |||||  |||||  |||||  |||||  |||||  
 481 sIleIlysIvalIleGluIysGlyTyrrArgGluIlysGlyIlnAlaIleG 498  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4542 CATTAAACGATGATGAAAGCTCACAGAAAGCTCACAGAAAGGCTAC 4497  
   |||||  |||||  |||||  |||||  |||||  |||||  
 498 LutYrsErGlyLeuIleuIgluIthrgIleuIleuIalathrgInLeuAla 514  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4496 ..TATAATGGATTAACAGAAACACAGTTCTGGGGCTACTCAGCTTGCT 4449  
   |||||  |||||  |||||  |||||  |||||  |||||  
 515 IleTyryrPheThrAspSerIleGluLeuAspIleGlyAspIleu... 529  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4448 ATCTTATTTTACAGACAGTCTGACTTAAACCTTAAACTTAA 4399  
   |||||  |||||  |||||  |||||  |||||  |||||  
 544 LavalAlaIlysIleuIgluItyrAlaIglnAspSerAsnProProgin 560  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4348 CTGTCATAAAAGATAATIACATGCTCAAAATGGCAGCCCCCAA 4299  
   |||||  |||||  |||||  |||||  |||||  |||||  
 561 LeuThrAspLeuAspPheIleProAsnAsnAspIstYrgIleserle 577  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4298 CTACAAATCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTGTTCT 4249  
   |||||  |||||  |||||  |||||  |||||  |||||  
 577 utIleGlyIthrGlnItrphsProGluaspIleuValAspIleLeuMetG 594  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4248 TATGGCAGATGCTCAGATGCTCAGATGCTCAGATGCTCAGATGCTCAG 4199  
   |||||  |||||  |||||  |||||  |||||  |||||  
 594 LysIplysIlys...GluValLeuProValThrHisasnLeuThrLeuArg 609  
   |||||  |||||  |||||  |||||  |||||  |||||  
 4198 AGATAAAAGCAAGAGTATTCCAGTCACAGTCAGTTGACAGRGAA 4149  
   |||||  |||||  |||||  |||||  |||||  |||||  
 610 LysThrValIleuIgluIleuIgluIgluIgluIgluIgluIgluIgluI 626  
   |||||  |||||  |||||  |||||  |||||  |||||



1084	GGGAGAGTCGAGCGAGAAAGAGCTAGATAGTTAGTAGGICACAGTTA	1084	MetArgGlnAlaLeuIysGlnLeuIleAspProAlaLeuIalathlysMe	236
1134	:        :    :    :    :    :    :    :    :    :	1134	ATGCAGCAGGATTGAAACACTTAATGATCCAAATTAGAGCTACTGC	1134
236	tProLySglnValProAspAspSpPheglNleSerIlePhegluSerGlu	253	253 sPlySgIyAspLystYrAsnIysGlyTyrgInasnIeuleSerGlyGly	269
1184	:    :    :    :    :    :    :    :    :    :    :	1184	:    :    :    :    :    :    :    :    :    :    :	1184
270	LeuValProThrLysProProThrProGlyAspPProProMetProProAs	286	270 LeuValProThrLysProProThrProGlyAspPProProMetProProAs	286
1217	TATGTACCTGTGATGATCCCTAACCTGGTGA	1260	1217 TATGTACCTGTGATGATCCCTAACCTGGTGA	1260
286	nGlnProGlnIhrIhrSerValLeuIleArgLystYrAlaLeuIleGlyAspT	303	286 nGlnProGlnIhrIhrSerValLeuIleArgLystYrAlaLeuIleGlyAspT	303
1261	:    :    :    :	1261	:    :    :    :	1261
1280	TAATCCCTAAACTCCCGAG	1318	1280 TAATCCCTAAACTCCCGAG	1318
316	GlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspI	332	316 GlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspI	332
1319	GATGATPATTGATGAACTACATGGGCCACTGATCTAGAT	1360	1319 GATGATPATTGATGAACTACATGGGCCACTGATCTAGAT	1360
332	eGlyGluArgIleGluLeuSerAspGlyLyrThrTyrThrLeuThrGluLeu	349	332 eGlyGluArgIleGluLeuSerAspGlyLyrThrTyrThrLeuThrGluLeu	349
1361	.GGTGAGAGAGTC	1382	1361 .GGTGAGAGAGTC	1382
349	snSerProAlaGlyTyrSerIleAlaGluProIleThrPhelysValGlu	365	349 snSerProAlaGlyTyrSerIleAlaGluProIleThrPhelysValGlu	365
1383	CAAGCCAGAGCTAGGCCCTGGCTTCCCCATTAAAGCCAGAG	1426	1383 CAAGCCAGAGCTAGGCCCTGGCTTCCCCATTAAAGCCAGAG	1426
366	AlaGlyLysValThrThrIleAspGlyLysGlnIle.. GluAsnPr	381	366 AlaGlyLysValThrThrIleAspGlyLysGlnIle.. GluAsnPr	381
1427	....TTAGATGGTCAGAGAGTCCTGAAAACC	1455	1427 ....TTAGATGGTCAGAGAGTCCTGAAAACC	1455
381	OasnIysGluIleValGluProTyrSerValGluAlaItyrasnAspPhe	398	381 OasnIysGluIleValGluProTyrSerValGluAlaItyrasnAspPhe	398
1456	TAGTATTGACTA.....CCTATGAGTCTCGTTATGAG..... 1492	1456 TAGTATTGACTA.....CCTATGAGTCTCGTTATGAG..... 1492	1456 TAGTATTGACTA.....CCTATGAGTCTCGTTATGAG..... 1492	
398	luGlubIheSerValLeuThrThrGlnAsnTyrAlaLysPhetYrTyrAla	414	398 luGlubIheSerValLeuThrThrGlnAsnTyrAlaLysPhetYrTyrAla	414
1492	.....	1492	1492 .....	1492
415	LysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLe	431	415 LysAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLe	431
1493	.....TTACAATTAAGA	1506	1493 .....	1506
431	UlysSerProProAPSPerGluAspGlyGlyLystYrMetThrPheAspP	448	431 UlysSerProProAPSPerGluAspGlyGlyLystYrMetThrPheAspP	448
1507	CCAACTCACCTCTAGCGGGTGA	1528	1507 CCAAATCACCTCTAGCGGGTGA	1528
448	hethrIhrHglyGluValWlysYr.. ThrHisIleIalaglyArgAspLeu	463	448 hethrIhrHglyGluValWlysYr.. ThrHisIleIalaglyArgAspLeu	463
1529	:    :    :    :    :    :    :    :    :    :    :    :	1570	:    :    :    :    :    :    :    :    :    :    :    :	1570
464	PhelysTyrThrValIysProArgAspThrAspProAspThrPheleLeuY	480	464 PhelysTyrThrValIysProArgAspThrAspProAspThrPheleLeuY	480
1571	.....CAGACCCGTTGATATGATAAA..... 1594	1571 .....	1571 .....	1571 .....
480	SHisIleLysIysValIleGluIysGlyTyArgGluIysGlyGlnAlaI	497	480 SHisIleLysIysValIleGluIysGlyTyArgGluIysGlyGlnAlaI	497
1595	.....AACTCCGAATGAAACAGGCTT..... TCAGGAATATGG	1631	1595 .....	1631
497	leGlyIurYrserGlyLeuThrIleGluIleArgAlaAlaIalathrGlnLeu	513	497 leGlyIurYrserGlyLeuThrIleGluIleArgAlaAlaIalathrGlnLeu	513
1632	TTGAGCAGAGAGATAGCAAAAGCAGAAGCTTGATGGAGGCCA.....	1678	1632 TTGAGCAGAGAGATAGCAAAAGCAGAAGCTTGATGGAGGCCA.....	1678
514	AlaIleItyrTyrIlePheThrAspSerAlaGluLeuAspIysAspIysLeu	530	514 AlaIleItyrTyrIlePheThrAspSerAlaGluLeuAspIysAspIysLeu	530
1679	.....AGTGAGTCGTTGAATTTACTAAAGACACTCAAAC	1713	1679 .....	1713
530	sAspTyrHisGly	534	530 sAspTyrHisGly	534
1714	AGCCATGAGTGGTCAAACAACTCTCACTGTTGAGACAGAAAGATACGAAAG	1763	1714 AGCCATGAGTGGTCAAACAACTCTCACTGTTGAGACAGAAAGATACGAAAG	1763
535	.....PheglAspMetAsnAspSerThrLeuAlavalAla	546	535 .....	546
1764	AGCCAGAAGTGTGATGGGGTCAAAGTGAGCT	1798	1764 AGCCAGAAGTGTGATGGGGTCAAAGTGAGCT	1798
547	LysIleLeuValGluItyrAlaGinAspSer.....	556	547 LysIleLeuValGluItyrAlaGinAspSer.....	556
1799	....GTGGAATTACTAAAGATACTCAACAGGCTATGGTGTCA	1839	1799 .....	1839
557	.AsnProProGlnIleLeuIleAspIysPhePheIleProAsnAsnL	573	557 .AsnProProGlnIleLeuIleAspIysPhePheIleProAsnAsnL	573
1840	ARCAACTCTAGATTGAGACAGACGAAAGGCCAAACATCCA	1882	1840 ARCAACTCTAGATTGAGACAGACGAAAGGCCAAACATCCA	1882
573	yStyrgIInSeerLeuIleGlyIhrGlnItpHisProGluAspLeuValAsp	589	573 yStyrgIInSeerLeuIleGlyIhrGlnItpHisProGluAspLeuValAsp	589
1882	.....	1882	1882 .....	1882
590	IleIleArgMetGluIysPlyIysGluValIleProvalThrHisAsnI	606	590 IleIleArgMetGluIysPlyIysGluValIleProvalThrHisAsnI	606
1883	....GTGTTGAGTGGGGCCAAAGTGAGTCGTTGATATTACT.....	1921	1883 .....	1921
606	uthrLeuIleArgLysThrValThrGlyLeuAlaItyraspArgThrIlysAspP	623	606 uthrLeuIleArgLysThrValThrGlyLeuAlaItyraspArgThrIlysAspP	623
623	heHisPheGluIleIleGluLeuIysAsnAsnIlysGin... GluIleLeu...	637	623 heHisPheGluIleIleGluLeuIysAsnAsnIlysGin... GluIleLeu...	637
1961	.....CAGGTGAGACAGAATACGAAGAGCCAGAGAAGAGITGTGATG	2002	1961 .....	2002
638	....SerGlnIhrValIlysthrAspIysThrAsnIleLeuIleGluPheIy	651	638 .....	651
2003	GGAGGTCAAGTCAGTCAGTCAGTCTGAATTACTAAACAGGCAT	2052	2003 GGAGGTCAAGTCAGTCAGTCAGTCTGAATTACTAAACAGGCAT	2052
651	SASPGLYIysAlaThrIleAsnIleIysHisGlyGluSerLeuThrIeug	668	651 SASPGLYIysAlaThrIleAsnIleIysHisGlyGluSerLeuThrIeug	668
2053	GATGGTCIACAAACACTCTCAGTTGAGACAGAGACACGAAAGGCCAG	2102	2053 GATGGTCIACAAACACTCTCAGTTGAGACAGAGACACGAAAGGCCAG	2102
668	InGlyLeuProGluIlyrTyrSerTyrLeuValIlytysGluThrAspSerGlu	684	668 InGlyLeuProGluIlyrTyrSerTyrLeuValIlytysGluThrAspSerGlu	684
2103	AAGGTGTTGAGGGAGGTCAAAGTGAGTCGTCGTTGATTA	2143	2103 AAGGTGTTGAGGGAGGTCAAAGTGAGTCGTCGTTGATTA	2143
685	GlyTyrylIysValAsnSerGlnIleValAlaAsnAlaIalathrValse	701	685 GlyTyrylIysValAsnSerGlnIleValAlaAsnAlaIalathrValse	701
2144	.....AAAGACACTCAACAGGATGAGTCGTTGATTTACT.....	713	2144 .....	713
701	rIysThrHglyIleThrSerAspGluThr.....LeuAlaI	713	701 rIysThrHglyIleThrSerAspGluThr.....LeuAlaI	713
2176	TGAACGCCGACTGTCGAGATAACGCCGAGAGATCGGAAAGCCTACAAA	2225	2176 TGAACGCCGACTGTCGAGATAACGCCGAGAGATCGGAAAGCCTACAAA	2225
713	heGluAsnIlys.....	717	713 heGluAsnIlys.....	717
2226	TGCAAAATAGGACCCAAAGTGAGAGAGATCGGAAAGCCTACAAA	2275	2226 TGCAAAATAGGACCCAAAGTGAGAGAGATCGGAAAGCCTACAAA	2275
731	yTyrLeuAlaLeuIleValIleAlaItyrIleSerIle	743	731 yTyrLeuAlaLeuIleValIleAlaItyrIleSerIle	743
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alignment\_block: US-09-494-297-2 x GGU31115 ..

Align seg 1/1 to: GGU31115 from: 1 to: 2066

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 318 ACRAAAAGAAAAMGGCATTGCGTGCAGACTTTAGGGAGCTTTAT 367  
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 462 TATCCCTCGTATGCTATGCTATACTGGAGCGTTTRAGAT.. 509  
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 794 GATTTGCTATATTCCTCTATAACTCAAGTTATA.. GTGGATGAGCT 840  
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 203 heIysArgIgUserGluUserAsnLeuValSerThrSerGlnIleLeuIeu 219  
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 841 GGAAGTCTGAATTAAGAGATGCGAGAAATTAGCGAAAGTCAGTAAGTTA 890  
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 1526 AACAGGCATGAGTGT..... 1541  
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 563 AspIleAspPheIleProAspAsnAsnIysTyrGlnSerLeuIleG 579  
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 1563 ACAGAAGATACGAAAGAGCCAGGA..... 1586  
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1438	ACAGGCTAGTGGTCGAAACACTCT.....CAGGTGAGAC	1675					
629	ulysAsnAsnlysGluGluLeuLeuSerGlnThrValLysThrAspLys	646					
1676	AGAGATACGAAAGAGCCAGGAGTGTAGTGCAGGCAAGTGAGCTG	1725					
646	hrAsnLeuGluPhelAspGlyLysAlaThrIleAsnLeuLysHISGLY	662					
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663	GluSerLeuThrLeuGlnGlyLeuProGluGlyTyroSerrTyLeuValy	679					
1764	TTCAGTCGAAACGCCAGGCTGTTGAGATAGCGTCGAGTTAGTGT	1813					
679	sGluThrAspSerGluGlyTyroLysValAsnSerGlnGluVala	696					
1814	CCATTGACAATAATGAGCCAAAGGGAAGAACATCAGGAAAACCTA	1863					
696	IaRsnAlaThrValSerLysHnGlyIleThSerAspGluThrLeuIa	712					
1864	CA.....CA.....CA.....CA.....CA.....CA.....CA.....	1865					
713	PheGluAsnAsnlysGluProValValPro...ThrGlyValAspGly	728					
1866	....AAATAATAACGACCTTCCTGCAACAGGAGATATGAGAA	1909					
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seq_documentation_block:							
DEFINITION	AF009914 321 bp DNA Streptococcus pyogenes fibronectin binding protein F gene, partial	13-FEB-1998					
ACCESSION	cds AF009914						
VERSION	AF009914.1	GI:2267181					
KEYWORDS	.						
SOURCE	Streptococcus pyogenes.						
ORGANISM	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus						
REFERENCE	1 (bases 1 to 321)						
AUTHORS	Katerov V., Andreev A., Schalen,C. and Totolian,A.A.						
TITLE	Protein F, a fibronectin-binding Protein of Streptococcus pyogenes, also binds human fibroningen: isolation of the protein and mapping of the binding region						
JOURNAL	Microbiology 144 (Pt 1), 119-126 (1998)						
MEDLINE	98129085						
REFERENCE	2 (bases 1 to 321)						
AUTHORS	Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A.						
TITLE	Direct Submission						
JOURNAL	Submitted (23-JUN-1997) Medical Microbiology, Lund University, Solvognaten 23, Lund 22562, Sweden						
FEATURES	Location/Qualifiers						
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		TITLE		Direct Submission	
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		FEATURES		Submitted Solvsgatan 23, Lund 22162, Sweden	
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VERSTON	AF009910.1	GI:	2267173		
KEYWORDS					
SOURCE	Streptococcus pyogenes.				
ORGANISM	Streptococcus pyogenes; Bacillus/Clostridium group; Streptococcaceae;				
REFERENCE	1 (bases 1 to 326)				
AUTHORS	Katerov, V., Andreev, A., Schalen, C. and Totolian, A.A.				
TITLE	Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: isolation of the protein and mapping of the binding region				
JOURNAL	Microbiology 144 (Pt 1), 119-126 (1998)				
MEDLINE	98129085				
REFERENCE	2 (bases 1 to 326)				
AUTHORS	Katerov, V.E., Andreev, A.S., Schalen, C. and Totolian, A.A.				
REFERENCE	1 (bases 1 to 348)				
seq_name: gb_ba1:AF009920					
seq_documentation_block:					
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ACCESSION	AF009920				
VERSTON	AF009920.1	GI:	2267193		
KEYWORDS	Streptococcus pyogenes.				
SOURCE	Streptococcus pyogenes; Bacillus/Clostridium group; Streptococcaceae;				
REFERENCE	1 (bases 1 to 348)				

AUTHORS Katerov,V., Andreev,A., Schalen,C. and Totolian,A.A.  
 TITLE Protein F, a fibronectin-binding protein of *Streptococcus pyogenes*,  
 also binds human fibrinogen: isolation of the protein and mapping  
 of the binding region  
 JOURNAL Microbiology 144 (Pt 1), 119-126 (1998)  
 MEDLINE 9812085  
 REFERENCE 2 (bases 1 to 348)  
 AUTHORS Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-1997) Medical Microbiology, Lund University,  
 Solvsgatan 23, Lund 22362, Sweden  
 FEATURES Location/Qualifiers  
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 . 62 easnProAspSerSerSerGluTyrrgtrrTyrgluserTyrv 79  
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 112 slysAlaPheProLeuGlySerAspSerSerValLysTrpTyrysl 129  
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 129 YSHISAspGlyLeuIleAsnGlnlysLeuArgAlaValMetTyrysl 162  
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 AUTHORS Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-1997) Medical Microbiology, Lund University,  
 Solvsgatan 23, Lund 22362, Sweden  
 FEATURES Location/Qualifiers  
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 . 62 easnProAspSerSerSerGluTyrrgtrrTyrgluserTyrv 79  
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 62 easnProAspSerSerSerGluTyrrgtrrTyrgluserTyrv 129  
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 79 alaRGlyHisProTyrrylysGlnpheArgValAlaIleAspLeuArg 95  
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 96 AAGGATTTGGCCAGGT.....CATGATTAAT 127  
 96 ValAsnLeuGluGlySerArgSerTyrglnValTyrcysPheAsnLeuLy 112  
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 128 GTCATTTACCGAGATTTAGAACGACATTAACTTAACTTACACGG 177  
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 ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 Streptococcus.  
 JOURNAL Microbiology 144 (Pt 1), 119-126 (1998)  
 MEDLINE 98129085  
 REFERENCE 1. (bases 1 to 310)  
 AUTHORS Katerov,V., Andreev,A., Schalen,C. and Totolian,A.A.  
 TITLE Protein F, a fibronectin-binding protein of Streptococcus pyogenes,  
 also binds human fibrinogen: isolation of the protein and mapping  
 of the binding region  
 2. (bases 1 to 310)  
 AUTHORS Katerov,V.E., Andreev,A.S., Schalen,C. and Totolian,A.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-1997) Medical Microbiology, Lund University,  
 Solvegatan 23, Lund 22362, Sweden  
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VERSION AF009919.1 GI:2267191

KEYWORDS SOURCE

ORGANISM Streptococcus pyogenes.

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococaceae;

REFERENCE STRPOTOCOCCUS

1 (bases 1 to 308) AUTHORS Katerov, V., Andreev, A., Schalen, C. and Totolian, A.A.

TITLE Protein F, a fibronectin-binding protein of Streptococcus pyogenes, also binds human fibrinogen: isolation of the protein and mapping

JOURNAL Microbiology 144 (Pt 1), 119-126 (1998)

MEDLINE 98129085

REFERENCE 2 (bases 1 to 308) AUTHORS Katerov, V.E., Andreev, A.S., Schalen, C. and Totolian, A.A.

TITLE Direct Submission JOURNAL Submitted (23-JUN-1997) Medical Microbiology, Lund University, Solvagatan 23, Lund 22266, Sweden

FEATURES SOURCE

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